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<http://workbench.sdsc.edu>

ALIGN

Optimal Global Sequence Alignment

- 51-02 SEQ ID NO:10 human mature BMP-11 NT
- 51-02 SEQ ID NO:1 bovine mature BMP-11 NT

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	10	20	30	40	50	60
51-02_SEQ_ID	AACCTGGGTCTGGACTGCGACGAGCACTCAAGCGAGTCCCCTGCTGCCGATATCCCCTC					
51-02_SEQ_ID
	10	20	30	40	50	60
	70	80	90	100	110	120
51-02_SEQ_ID	ACAGTGGACTTTGAGGCTTTTCGGCTGGGACTGGATCATCGCACCTAAGCGCTACAAGGCC					
51-02_SEQ_ID	::
	70	80	90	100	110	120
	130	140	150	160	170	180
51-02_SEQ_ID	AACTACTGCTCCGGCCAGTGCGAGTACATGTTTCATGCAAAATATCCGCATACCCATTG					
51-02_SEQ_ID
	130	140	150	160	170	180
	190	200	210	220	230	240
51-02_SEQ_ID	GTGCAGCAGGCCAATCCAAGAGGCTCTGCTGGGCCCTGTTGTACCCCCACCAAGATGTCC					
51-02_SEQ_ID
	190	200	210	220	230	240
	250	260	270	280	290	300
51-02_SEQ_ID	CCAATCAACATGCTCTACTTCAATGACAAGCAGCAGATTATCTACGGCAAGATCCCTGGC					
51-02_SEQ_ID
	250	260	270	280	290	300
	310	320				

```
51-02_SEQ_ID  ATGGTGGTGGATCGCTGTGGCTGCTCT
               :
51-02_SEQ_ID  ATGGTGGTGGATCGCTGTGGCTGCTCC
               310       320
```

Import Alignment(s)	Return	Help	Report Bugs
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Citation

Algorithm Citation:

E. W. Myers and W. Miller, (1989) CABIOS 4:11-17.

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448.

W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology 183:63-98).

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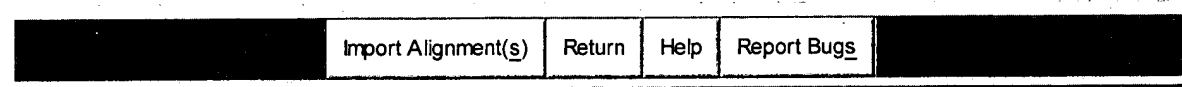
                250      260      270      280      290      300
SEQ_ID_NO:1_   TTCAATGACAAGCAGCAGATTATCTACGGCAAGATCCCTGGCATGGTGGTGGATCGCTGT
                :
                :
                :
SEQ_ID_NO:10   TTCAATGACAAGCAGCAGATTATCTACGGCAAGATCCCTGGCATGGTGGTGGATCGCTGT
                250      260      270      280      290      300

```

```

SEQ_ID_NO:1_   GGCTGC
                :
                :
SEQ_ID_NO:10   GGCTGC

```



Citation

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